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Short Communication

Mapping the global geographic potential of Coronavirus Disease 19 (COVID-19)

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Abstract. The World are presently experiencing the most serious known outbreak of Coronavirus Disease 2019 (COVID-19) in 2020. COVID-19 is an outbreak detected in Wuhan City, China. We use ecological niche models to predict the potential distribution of the dispersion of COVID-19 in the World. We use 140 records of infected people as an approximation for the construction of ecological niche models using a recent methodology to have a better interpretation of the

results. The study addresses urgent knowledge gaps regarding (1) the potential geographic scope of the current COVID-19 epidemic, and (2) the global potential for spread of COVID-19. Our results demonstrate the dispersion of COVID-19 in the world, and we have very little uncertainty in certain areas of the world. The results can be extrapolated and can also serve as an alert for countries where there are no cases of the disease.

Key words: Coronavirus Diseases 19, global distribution, ecological niche modeling, accessibility, spread

Introduction

Coronavirus Disease 2019 (COVID-19) is an outbreak of respiratory disease caused by a novel (new) coronavirus detected in Wuhan City, Hubei Province, China (Lin et al. 2020) and which has now been detected in 40 locations internationally (NIH 2020). On January 30, 2020, the International Health Regulations Emergency Committee of the World Health Organization declared the outbreak a “public health emergency of international concern”. Coronaviruses are a large family of viruses that are common in many different species of animals, including camels, cattle, cats, and bats. Rarely, animal coronaviruses can infect people and the spread between people such as with MERS-CoV, SARS-CoV and now with this new virus (COVID-2019) (NIH 2020). Ecological niche models have been used to predict the potential coronavirus distribution as MERS-CoV (Samy & Peterson 2015). The objective of this study is to provide an approximation of the dispersion of the global geographic distribution of COVID-19 using ecological niche models.

Material and Methods

A database was compiled of web site of Johns Hopkins University based dashboard to track COVID-19 in real time (Dong et al. 2020). A final total of 140 unique occurrence sites were included in the database, while duplicate occurrences were eliminated to reduce effects of spatial autocorrelation by thinning records within 5km of individual occurrence points using the spThin R package (Ailello-Lammens et al., 2015). Model significance was analyzed by setting aside 65% of data points for model calibration, 25% for internal testing, and 10% for final

evaluation as described by Muscarella et al. (2014). Fifteen bioclimatic layers (1970-2000) were used to construct ENM from the WorldClim database version 2.0 (Fick and Hijmans, 2017; available: <http://www.worldclim.org>), excluding those that combine temperature (Bio08 and Bio09) and precipitation (Bio18 and Bio19) owing to known artifacts (Escobar et al., 2014). Variables for the climate model were used for 2.5 minutes spatial resolution (approximately 5 km X 5 km per pixel), which is adequately coarse for climate influences on species distributions (Pearson and Dawson, 2003). We used three sets of environmental predictors: (Set1) 15 variables from WorldClim; (Set2) a jackknife process in MaxEnt was used to select distinct sets of variables that contributed most to models (>90%); and (Set3) a jackknife process in MaxEnt was used and correlation analyses performed to select variable sets that contributed most to models (>90%), eliminating one variable per pair if the Pearson correlation was $r < 0.8$ (Moo-Llanes et al., 2013). Ecological niche was modelled using the maximum entropy (MaxEnt) algorithm based on the kuenm R package (Cobos et al., 2019). For COVID19, we created candidate models by combining three sets of environmental variables, 17 values of regularization multiplier (0.1–1 with intervals of 0.1, 2–6 with intervals of 1, 8, and 10), and all 29 possible combinations of 5 feature classes (linear = l, quadratic = q, product = p, threshold = t, and hinge = h) (Cobos et al., 2019). The model performance and best candidate models were selected first by significance, second by performance and subsequently by AIC: AICCc, Delta AICCc and Weight AICCc. The final model and its evaluation were generated by bootstrap for each haplogroup using 10 replicates with logistic outputs, and these were transferred to the current (Cobos et al., 2019). To identify geographically high-risk areas for model

transfer using environmental distances between sites generally and to the nearest portion of the calibration region using Mobility-Oriented Parity (MOP) analyses, we compared environmental breadth of predictors within **M** (10% reference points sampled) for COVID19.

Results and Discussion

An important premise for the results is that COVID19 cannot build an accessible area **M** (Barve et al. 2011) for the delimitation of its potential distribution, due to the form of transmission from person to person. In a binary map we can see that 60% of the world territory presents the optimal conditions for the development and propagation of COVID19. A total of 1,479 candidate models were built for this species, while 207 models were statistically significant. Finally, one candidate model was statistically significant meeting omission rate and AICc criteria. The best candidate model was model with set environmental predictors (Set2), regularization multiple (N=2.0), feature classes (quadratic), mean AUC ratio (N=1.00), partial ROC (N=0.00), omission rate 5% (N=0.00), Akaike Information Criterion corrected (N=1,112.06), Delta Akaike Information Criterion corrected (N=0.00), Akaike Information Criterion corrected weight (N=0.74) and number parameters (N=6). The Bio02 (Mean diurnal range) and Bio01 (Annual mean temperature) gives estimates of relative contributions of the environmental variables to the Maxent model. Ecological niche modeling for COVID19 was suitability between 0.04 to 0.54. The model was projected for worldwide. We can observe the dispersion of COVID-19 throughout Latin America, including United States, Africa, greatest part of Europe, Oceania and the South Asia region. MOP

results suggest a portion is observed for a strict extrapolation in large part worldwide; compared to minimum values from 0.0001 to 0.086 in the north part of the world (Fig. 1). Finally, our results agree with the sites of the potential distribution of COVID-19 worldwide. Ecological niche models have been widely used in other diseases both at the outbreak level (Samy & Peterson 2015) and endemic diseases of a certain region (Peterson et al. 2017). We hope that these results will serve as an alert measure for countries where there are no cases of COVID-19 and have a better mitigation and control strategy for this disease.

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CRedit authorship contribution statement

David A. Moo-Llanes: Conceptualization, Investigation, Formal analysis, Investigation, Writing - original draft, Writing - review & editing.

Declaration of Competing Interest

None

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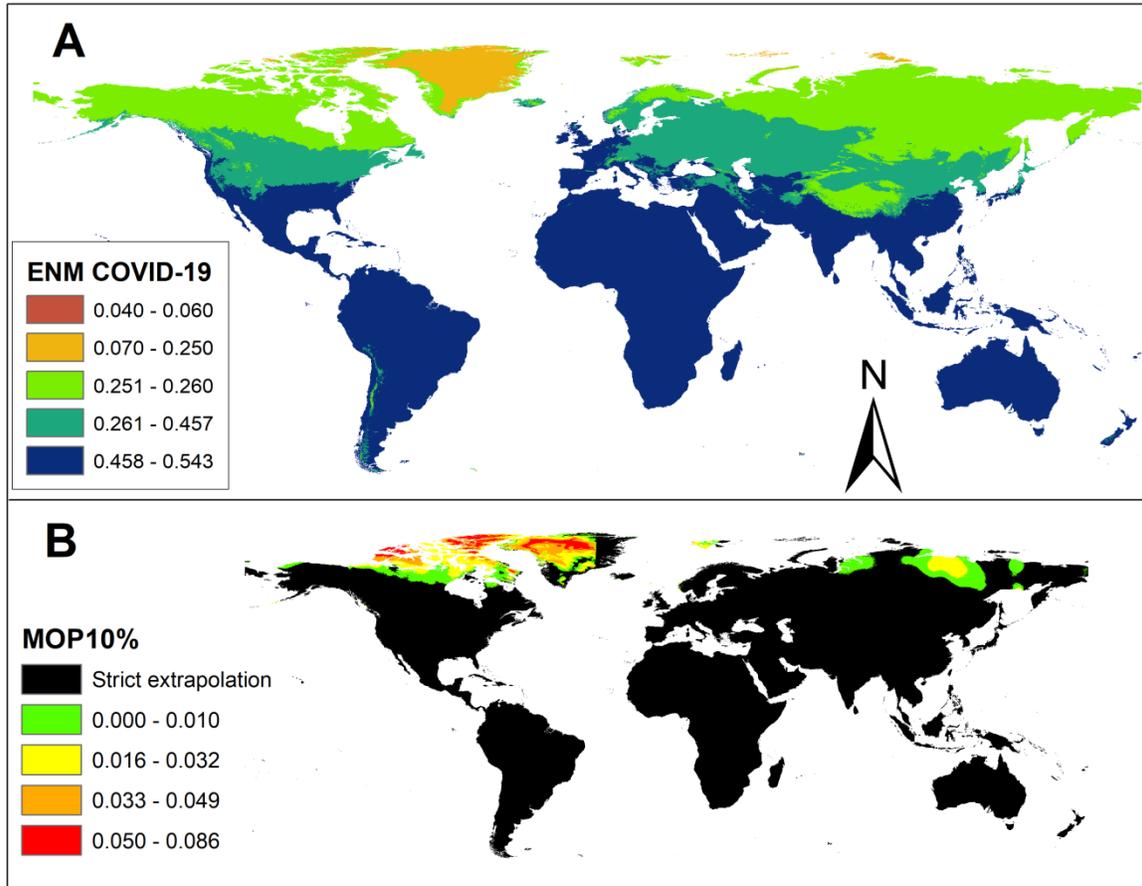


Figure 1. Ecological Niche Modeling suitability and MOP10%for COVID19.

a) Ecological niche modeling; b) MOP 10% analysis